#8

RAW SEQUENCE LISTING   DATE: 10/18/2001
PATENT APPLICATION: US/09/432,503   TIME: 09:34:58

Input Set : N:\Crf3\RULE60\09432503.txt
Output Set: N:\CRF3\10182001\I432503.raw

```
                SEQUENCE LISTING
 4  (1) GENERAL INFORMATION:
 6       (i) APPLICANT: Cech, Thomas R.
 7                      Lingner, Joachim
 8                      Nakamura, Toru
 9                      Chapman, Karen B.
10                      Morin, Gregg B.
11                      Harley, Calvin B.
12                      Andrews, William H.
14      (ii) TITLE OF INVENTION: Human Telomerase Catalytic Subunit
16     (iii) NUMBER OF SEQUENCES: 727
18      (iv) CORRESPONDENCE ADDRESS:
19           (A) ADDRESSEE: Townsend and Townsend and Crew LLP
20           (B) STREET: Two Embarcadero Center, Eighth Floor
21           (C) CITY: San Francisco
22           (D) STATE: California
23           (E) COUNTRY: USA
24           (F) ZIP: 94111-3834
26       (v) COMPUTER READABLE FORM:
27           (A) MEDIUM TYPE: Floppy disk
28           (B) COMPUTER: IBM PC compatible
29           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
32      (vi) CURRENT APPLICATION DATA:
C--> 33      (A) APPLICATION NUMBER: US/09/432,503
C--> 34      (B) FILING DATE: 02-Nov-1999
35           (C) CLASSIFICATION:
73     (vii) PRIOR APPLICATION DATA:
38           (A) APPLICATION NUMBER: 08/974,549
39           (B) FILING DATE:
42           (A) APPLICATION NUMBER: US 08/844,419
43           (B) FILING DATE: 18-APR-1997
46           (A) APPLICATION NUMBER: US 08/846,017
47           (B) FILING DATE: 25-APR-1997
50           (A) APPLICATION NUMBER: US 08/851,843
51           (B) FILING DATE: 06-MAY-1997
54           (A) APPLICATION NUMBER: US 08/854,050
55           (B) FILING DATE: 09-MAY-1997
58           (A) APPLICATION NUMBER: US 08/911,312
59           (B) FILING DATE: 14-AUG-1997
62           (A) APPLICATION NUMBER: US 08/912,951
63           (B) FILING DATE: 14-AUG-1997
66           (A) APPLICATION NUMBER: US 08/915,503
67           (B) FILING DATE: 14-AUG-1997
70           (A) APPLICATION NUMBER: WO PCT/US97/17618
71           (B) FILING DATE: 01-OCT-1997
74           (A) APPLICATION NUMBER: WO PCT/US97/17885
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75            (B) FILING DATE: 01-OCT-1997
77    (viii) ATTORNEY/AGENT INFORMATION:
78            (A) NAME: Apple, Randolph Ted
79            (B) REGISTRATION NUMBER: 36,429
80            (C) REFERENCE/DOCKET NUMBER: 015389-002610US
82     (ix) TELECOMMUNICATION INFORMATION:
83            (A) TELEPHONE: (415) 576-0200
84            (B) TELEFAX: (415) 576-0300
87 (2) INFORMATION FOR SEQ ID NO: 1:
89      (i) SEQUENCE CHARACTERISTICS:
90            (A) LENGTH: 4015 base pairs
91            (B) TYPE: nucleic acid
92            (C) STRANDEDNESS: single
93            (D) TOPOLOGY: linear
95     (ii) MOLECULE TYPE: cDNA
98     (ix) FEATURE:
99            (A) NAME/KEY: CDS
100           (B) LOCATION: 56..3454
101           (D) OTHER INFORMATION: /product= "hTRT"
102 /note= "human telomerase reverse
103 transcriptase (hTRT) catalytic protein
104 component"
107     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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110                                                                 Met
111                                                                   1
113 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC     106
114 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
115              5               10                  15
117 TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC     154
118 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
119          20              25                  30
121 CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG     202
122 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
123      35              40                  45
125 CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC     250
126 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
127  50              55              60                  65
129 CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG     298
130 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
131              70              75                  80
133 GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG     346
134 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
135              85              90                  95
137 GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG     394
138 Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
139          100             105                 110
141 GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC     442
142 Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp
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145 GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC    490
146 Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
147 130                   135                   140             145
149 GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG    538
150 Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
151               150                   155                   160
153 GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG    586
154 Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
155               165                   170                   175
157 CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC    634
158 Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
159         180                   185                   190
161 CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG    682
162 Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
163     195                   200                   205
165 GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG    730
166 Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
167 210                   215                   220             225
169 GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC    778
170 Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
171               230                   235                   240
173 GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC    826
174 Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
175            '245                   250                   255
177 CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG    874
178 His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
179         260                   265                   270
181 TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC    922
182 Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
183     275                   280                   285
185 TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG    970
186 Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
187 290                   295                   300             305
189 GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT    1018
190 Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys
191               310                   315                   320
193 CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC    1066
194 Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
195               325                   330                   335
197 AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC    1114
198 Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser
199         340                   345                   350
201 CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG    1162
202 Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg
203     355                   360                   365
205 CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC    1210
206 Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg
207 370                   375                   380             385
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209 TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG     1258
210 Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala
211              390             395                 400
213 CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT     1306
214 Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala
215              405             410                 415
217 GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC     1354
218 Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly
219              420             425                 430
221 TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG     1402
222 Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val
223      435             440                 445
225 CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG     1450
226 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
227 450                 455                 460             465
229 CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG     1498
230 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
231              470             475                 480
233 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG     1546
234 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
235              485             490                 495
237 GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC     1594
238 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
239          500             505                 510
241 GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT     1642
242 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
243      515             520                 525
245 CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG     1690
246 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
247 530             535                 540             545
249 CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT     1738
250 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
251              550             555                 560
253 TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG     1786
254 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
255              565             570                 575
257 AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG     1834
258 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
259          580             585                 590
261 AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT     1882
262 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
263      595             600                 605
265 CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC     1930
266 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
267 610             615                 620                 625
269 AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA     1978
270 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
271              630             635                 640
273 GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG     2026
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274 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
275             645             650             655
277 GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC        2074
278 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
279         660             665             670
281 GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC        2122
282 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
283     675             680             685
285 TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG        2170
286 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
287 690             695             700             705
289 CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC        2218
290 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
291             710             715             720
293 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC        2266
294 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
295             725             730             735
297 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG        2314
298 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
299         740             745             750
301 CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC        2362
302 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
303     755             760             765
305 CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG        2410
306 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
307 770             775             780             785
309 CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC        2458
310 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
311             790             795             800
313 AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC        2506
314 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
315             805             810             815
317 GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG        2554
318 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
319         820             825             830
321 GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG        2602
322 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
323     835             840             845
325 GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT      ' 2650
326 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
327 850             855             860             865
329 TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA        2698
330 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
331             870             875             880
333 ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG        2746
334 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
335             885             890             895
337 GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC        2794
338 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
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                  VERIFICATION SUMMARY                DATE: 10/18/2001
                  PATENT APPLICATION:  US/09/432,503  TIME: 09:34:59

                    Input Set : N:\Crf3\RULE60\09432503.txt
                    Output Set: N:\CRF3\10182001\I432503.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
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L:1968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
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L:2920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:4392 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=105
L:4414 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=106
L:4437 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=107
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L:4459 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=108
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L:5302 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 111
L:5583 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=114
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L:8053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:197
L:8093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:198
L:8149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199
L:8562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:214
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L:11804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293
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VERIFICATION SUMMARY   DATE: 10/18/2001
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Input Set : N:\Crf3\RULE60\09432503.txt
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L:14800 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=385
L:14822 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=386
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L:14910 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=390
L:14932 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=391
L:14954 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=392
L:14976 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=393
L:14998 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=394
L:15020 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=395
L:15042 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=396
L:15064 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=397
L:15086 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=398
L:15108 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=399
```

Input Set : N:\Crf3\RULE60\09432503.txt
Output Set: N:\CRF3\10182001\I432503.raw

L:15130 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=400
L:15152 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=401
L:15174 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=402
L:15196 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=403
L:15218 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=404
L:15240 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=405
L:15262 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=406
L:15284 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=407
L:15306 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=408